RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: _____ 10/763, 976 B _____

Source: _____ IFW16 _____

Date Processed by STIC: _____ 04/05/2007 _____

ENTERED

RAW SEQUENCE LISTING   DATE: 04/05/2007
PATENT APPLICATION: US/10/763,976B   TIME: 10:25:18

Input Set : A:\960296.00463.txt
Output Set: N:\CRF4\04052007\J763976B.raw

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 3 <110> APPLICANT: Harms, Jerome S
 4        Splitter, Gary A
 5        Eakle, Kurt A
 6        Bremel, Robert D
 8 <120> TITLE OF INVENTION: INDUCIBLE PROTEIN EXPRESSION SYSTEM
10 <130> FILE REFERENCE: 960296.00463
12 <140> CURRENT APPLICATION NUMBER: 10/763,976B
13 <141> CURRENT FILING DATE: 2004-01-23
15 <150> PRIOR APPLICATION NUMBER: US 60/442,103
16 <151> PRIOR FILING DATE: 2003-01-23
18 <160> NUMBER OF SEQ ID NOS: 29
20 <170> SOFTWARE: PatentIn version 3.3
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 480
24 <212> TYPE: DNA
25 <213> ORGANISM: Artificial
27 <220> FEATURE:
28 <223> OTHER INFORMATION: Engineered sequence from virus and plasmid
31 <220> FEATURE:
32 <221> NAME/KEY: promoter
33 <222> LOCATION: (87)..(432)
34 <223> OTHER INFORMATION: BLV promoter
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39 atggccgctt tggtcgaggc ggatcctagc agaaaaataa gacttgattc ccccttaaaa     120
41 ttacaactgc tagaaaatga atggctctcc cgcctttttt gagggggaat catttgtatg     180
43 aaagatcatg ccgacctagg cgccgccacc gccccgtaaa ccagacagag acgtcagctg     240
45 ccagaaaagc tggtgacggc agctggtggc tagaatcccc gtacctcccc aacttcccct     300
47 ttcccgaaaa atccacaccc tgagctgctg acctcacctg ctgataaatt aataaaatgc     360
49 cggccctgtc gagttagcgg caccagaagc gttcttctcc tgagaccctc gtgctcagct     420
51 ctcggtcctg cctcgagaag cttgttatca caagtttgta caaaaaagct gaacgagaaa     480
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55 <211> LENGTH: 929
56 <212> TYPE: DNA
57 <213> ORGANISM: Bovine leukemia virus
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61 <221> NAME/KEY: CDS
62 <222> LOCATION: (1)..(927)
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67 1               5                   10                  15
69 gcc ctg gtt ttg tcc aat gac gtc acc atc gat gcc tgg tgc ccc ctc       96
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70 Ala Leu Val Leu Ser Asn Asp Val Thr Ile Asp Ala Trp Cys Pro Leu
71         20              25              30
73 tgc ggg ccc cat gag cga ctc caa ttc gaa agg atc gac acc acg cac    144
74 Cys Gly Pro His Glu Arg Leu Gln Phe Glu Arg Ile Asp Thr Thr His
75         35              40              45
77 acc tgc gag acc cac cgt atc acc tgg acc gcc gat gga cga cct ttc    192
78 Thr Cys Glu Thr His Arg Ile Thr Trp Thr Ala Asp Gly Arg Pro Phe
79     50              55              60
81 ggc ctc aat gga gcg ctg ttc cct cga ctg cat gtc tcc aga gac ccg    240
82 Gly Leu Asn Gly Ala Leu Phe Pro Arg Leu His Val Ser Arg Asp Pro
83 65              70              75              80
85 gcc cca agg gcc cga cga ctc tgg atc aac tgc ccc ctt ccg gcc gtt    288
86 Ala Pro Arg Ala Arg Arg Leu Trp Ile Asn Cys Pro Leu Pro Ala Val
87             85              90              95
89 cgc gct cag ccc ggc ccg gtt tca ctt tcc ccc ttc gag cgg tcc ccc    336
90 Arg Ala Gln Pro Gly Pro Val Ser Leu Ser Pro Phe Glu Arg Ser Pro
91             100             105             110
93 ttc cag ccc tac caa tgc caa ttg ccc tcg gcc tct agc gac ggt tgc    384
94 Phe Gln Pro Tyr Gln Cys Gln Leu Pro Ser Ala Ser Ser Asp Gly Cys
95         115             120             125
97 ccc gtc atc ggg cac ggc ctt ctt ccc tgg aac aac tta gta acg cat    432
98 Pro Val Ile Gly His Gly Leu Leu Pro Trp Asn Asn Leu Val Thr His
99     130             135             140
101 cct tgt cct cgg aaa gtc ctt ata tta aat caa atg gcc aat ttt tcc    480
102 Pro Cys Pro Arg Lys Val Leu Ile Leu Asn Gln Met Ala Asn Phe Ser
103 145             150             155             160
105 tta ctc ccc ccc ttc aat acc ctc ctt gtg gac ccc ctc cgg ttg tcc    528
106 Leu Leu Pro Pro Phe Asn Thr Leu Leu Val Asp Pro Leu Arg Leu Ser
107             165             170             175
109 gtc ttt gcc cca gac acc agg gga gcc ata cgt tat ctc tcc acc ctt    576
110 Val Phe Ala Pro Asp Thr Arg Gly Ala Ile Arg Tyr Leu Ser Thr Leu
111             180             185             190
113 ttg acg cta tgc cca gct act tgt att cta ccc ctc ggc gag ccc ttc    624
114 Leu Thr Leu Cys Pro Ala Thr Cys Ile Leu Pro Leu Gly Glu Pro Phe
115         195             200             205
117 tct cct aat gtc ccc ata tgt cgc ttt ccc cgg gac tcc aat gaa ccc    672
118 Ser Pro Asn Val Pro Ile Cys Arg Phe Pro Arg Asp Ser Asn Glu Pro
119     210             215             220
121 ccc ctt tca gaa ttc gag ctg ccc ctt atc caa acg ccc ggc ctg tct    720
122 Pro Leu Ser Glu Phe Glu Leu Pro Leu Ile Gln Thr Pro Gly Leu Ser
123 225             230             235             240
125 tgg tct gtc ccc gcg atc gac cta ttc cta acc ggc ccc cct tcc cca    768
126 Trp Ser Val Pro Ala Ile Asp Leu Phe Leu Thr Gly Pro Pro Ser Pro
127             245             250             255
129 tgc gac cgg tta cac gta tgg tcc agt cct cag gcc tta cag cgc ttc    816
130 Cys Asp Arg Leu His Val Trp Ser Ser Pro Gln Ala Leu Gln Arg Phe
131             260             265             270
133 ctc cat gac cct acg cta acc tgg tca gaa ttg gtt gct agc agg aaa    864
134 Leu His Asp Pro Thr Leu Thr Trp Ser Glu Leu Val Ala Ser Arg Lys
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135          275                280                285
137 cta aga ctt gat tca ccc tta aaa tta caa ctg tta gaa aat gaa tgg          912
138 Leu Arg Leu Asp Ser Pro Leu Lys Leu Gln Leu Leu Glu Asn Glu Trp
139      290                295                300
141 ctc tcc cgc ctt ttt tg                                                    929
142 Leu Ser Arg Leu Phe
143 305
146 <210> SEQ ID NO: 3
147 <211> LENGTH: 309
148 <212> TYPE: PRT
149 <213> ORGANISM: Bovine leukemia virus
151 <400> SEQUENCE: 3
153 Met Ala Ser Val Val Gly Trp Gly Pro His Ser Leu His Ala Cys Pro
154 1               5                10               15
157 Ala Leu Val Leu Ser Asn Asp Val Thr Ile Asp Ala Trp Cys Pro Leu
158          20               25               30
161 Cys Gly Pro His Glu Arg Leu Gln Phe Glu Arg Ile Asp Thr Thr His
162          35               40               45
165 Thr Cys Glu Thr His Arg Ile Thr Trp Thr Ala Asp Gly Arg Pro Phe
166      50               55               60
169 Gly Leu Asn Gly Ala Leu Phe Pro Arg Leu His Val Ser Arg Asp Pro
170 65               70               75               80
173 Ala Pro Arg Ala Arg Arg Leu Trp Ile Asn Cys Pro Leu Pro Ala Val
174          85               90               95
177 Arg Ala Gln Pro Gly Pro Val Ser Leu Ser Pro Phe Glu Arg Ser Pro
178          100              105              110
181 Phe Gln Pro Tyr Gln Cys Gln Leu Pro Ser Ala Ser Ser Asp Gly Cys
182          115              120              125
185 Pro Val Ile Gly His Gly Leu Leu Pro Trp Asn Asn Leu Val Thr His
186      130              135              140
189 Pro Cys Pro Arg Lys Val Leu Ile Leu Asn Gln Met Ala Asn Phe Ser
190 145              150              155              160
193 Leu Leu Pro Pro Phe Asn Thr Leu Leu Val Asp Pro Leu Arg Leu Ser
194          165              170              175
197 Val Phe Ala Pro Asp Thr Arg Gly Ala Ile Arg Tyr Leu Ser Thr Leu
198          180              185              190
201 Leu Thr Leu Cys Pro Ala Thr Cys Ile Leu Pro Leu Gly Glu Pro Phe
202          195              200              205
205 Ser Pro Asn Val Pro Ile Cys Arg Phe Pro Arg Asp Ser Asn Glu Pro
206      210              215              220
209 Pro Leu Ser Glu Phe Glu Leu Pro Leu Ile Gln Thr Pro Gly Leu Ser
210 225              230              235              240
213 Trp Ser Val Pro Ala Ile Asp Leu Phe Leu Thr Gly Pro Pro Ser Pro
214          245              250              255
217 Cys Asp Arg Leu His Val Trp Ser Ser Pro Gln Ala Leu Gln Arg Phe
218          260              265              270
221 Leu His Asp Pro Thr Leu Thr Trp Ser Glu Leu Val Ala Ser Arg Lys
222      275              280              285
225 Leu Arg Leu Asp Ser Pro Leu Lys Leu Gln Leu Leu Glu Asn Glu Trp
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226      290                  295                  300
229 Leu Ser Arg Leu Phe
230 305
233 <210> SEQ ID NO: 4
234 <211> LENGTH: 1062
235 <212> TYPE: DNA
236 <213> ORGANISM: Human T-cell lymphotropic virus type 1
239 <220> FEATURE:
240 <221> NAME/KEY: CDS
241 <222> LOCATION: (1)..(1062)
243 <220> FEATURE:
244 <221> NAME/KEY: promoter
245 <222> LOCATION: (1)..(353)
247 <400> SEQUENCE: 4
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250 1               5                   10                  15
252 gtc tac gtg ttt gga gac ggc gac tgg tgc ccc tgt gta caa atc tct      96
253 Val Tyr Val Phe Gly Asp Gly Asp Trp Cys Pro Cys Val Gln Ile Ser
254                 20                  25                  30
256 ggg gga cta tgt tcg gcc cgc cta cat cgt cac gcc cta ctg gcc acc     144
257 Gly Gly Leu Cys Ser Ala Arg Leu His Arg His Ala Leu Leu Ala Thr
258             35                  40                  45
260 tgt cca gag cat cag atc acc tgg gac ccc atc gat gga cgc gtt atc     192
261 Cys Pro Glu His Gln Ile Thr Trp Asp Pro Ile Asp Gly Arg Val Ile
262     50                  55                  60
264 ggc tca gct cta cag ttc ctt atc cct cga ctc ccc tcc ttc ccc acc     240
265 Gly Ser Ala Leu Gln Phe Leu Ile Pro Arg Leu Pro Ser Phe Pro Thr
266 65                  70                  75                  80
268 cag aga acc tct aag acc ctc aag gtc ctt acc ccg cca atc act cat     288
269 Gln Arg Thr Ser Lys Thr Leu Lys Val Leu Thr Pro Pro Ile Thr His
270                 85                  90                  95
272 aca acc ccc aac att cca ccc tcc ttc ctc cag gcc atg cgc aaa tac     336
273 Thr Thr Pro Asn Ile Pro Pro Ser Phe Leu Gln Ala Met Arg Lys Tyr
274                 100                 105                 110
276 tcc ccc ttc cga aat gga tac atg gaa ccc acc ctt ggg cag cac ctc     384
277 Ser Pro Phe Arg Asn Gly Tyr Met Glu Pro Thr Leu Gly Gln His Leu
278             115                 120                 125
280 cca acc ctg tct ttt cca gac ccc gga ctc cgg ccc caa aac ctg tac     432
281 Pro Thr Leu Ser Phe Pro Asp Pro Gly Leu Arg Pro Gln Asn Leu Tyr
282     130                 135                 140
284 acc ctc tgg gga ggc tcc gtt gtc tgc atg tac ctc tac cag ctt tcc     480
285 Thr Leu Trp Gly Gly Ser Val Val Cys Met Tyr Leu Tyr Gln Leu Ser
286 145                 150                 155                 160
288 ccc ccc atc acc tgg ccc ctc ctg ccc cac gtg att ttt tgc cac ccc     528
289 Pro Pro Ile Thr Trp Pro Leu Leu Pro His Val Ile Phe Cys His Pro
290                 165                 170                 175
292 ggc cag ctc ggg gcc ttc ctc acc aat gtt ccc tac aag cga ata gaa     576
293 Gly Gln Leu Gly Ala Phe Leu Thr Asn Val Pro Tyr Lys Arg Ile Glu
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294            180            185            190
296 gaa ctc ctc tat aaa att tcc ctt acc aca ggg gcc cta ata att cta    624
297 Glu Leu Leu Tyr Lys Ile Ser Leu Thr Thr Gly Ala Leu Ile Ile Leu
298        195            200            205
300 ccc gaa gac tgt ttg ccc acc acc ctt ttc cag cct gtt agg gca ccc    672
301 Pro Glu Asp Cys Leu Pro Thr Thr Leu Phe Gln Pro Val Arg Ala Pro
302        210            215            220
304 gtc acg cta aca gcc tgg caa aac ggc ctc ctt ccg ttc cac tca acc    720
305 Val Thr Leu Thr Ala Trp Gln Asn Gly Leu Leu Pro Phe His Ser Thr
306 225            230            235            240
308 ctc acc act cca ggc ctt att tgg aca ttt acc gat ggc acg cct atg    768
309 Leu Thr Thr Pro Gly Leu Ile Trp Thr Phe Thr Asp Gly Thr Pro Met
310            245            250            255
312 att tcc ggg ccc tgc cct aaa gat ggc cag cca tct tta gta cta cag    816
313 Ile Ser Gly Pro Cys Pro Lys Asp Gly Gln Pro Ser Leu Val Leu Gln
314            260            265            270
316 tcc tcc tcc ttt ata ttt cac aaa ttt caa acc aag gcc tac cac ccc    864
317 Ser Ser Ser Phe Ile Phe His Lys Phe Gln Thr Lys Ala Tyr His Pro
318        275            280            285
320 tca ttt cta ctc tca cac ggc ctc ata cag tac tct tcc ttt cat aat    912
321 Ser Phe Leu Leu Ser His Gly Leu Ile Gln Tyr Ser Ser Phe His Asn
322        290            295            300
324 tta cat ctc ctg ttt gaa gaa tac acc aac atc ccc att tct cta ctt    960
325 Leu His Leu Leu Phe Glu Glu Tyr Thr Asn Ile Pro Ile Ser Leu Leu
326 305            310            315            320
328 ttt aac aaa aaa gag gca gat gac aat gac cat gag ccc caa ata tcc    1008
329 Phe Asn Lys Lys Glu Ala Asp Asp Asn Asp His Glu Pro Gln Ile Ser
330            325            330            335
332 ccc ggg ggc tta gag cct ccc agt gaa aaa cat ttc cgc gaa aca gaa    1056
333 Pro Gly Gly Leu Glu Pro Pro Ser Glu Lys His Phe Arg Glu Thr Glu
334            340            345            350
336 gtc tga                                                            1062
337 Val
341 <210> SEQ ID NO: 5
342 <211> LENGTH: 353
343 <212> TYPE: PRT
344 <213> ORGANISM: Human T-cell lymphotropic virus type 1
346 <400> SEQUENCE: 5
348 Met Ala His Phe Pro Gly Phe Gly Gln Ser Leu Leu Phe Gly Tyr Pro
349 1            5            10            15
352 Val Tyr Val Phe Gly Asp Gly Asp Trp Cys Pro Cys Val Gln Ile Ser
353        20            25            30
356 Gly Gly Leu Cys Ser Ala Arg Leu His Arg His Ala Leu Leu Ala Thr
357        35            40            45
360 Cys Pro Glu His Gln Ile Thr Trp Asp Pro Ile Asp Gly Arg Val Ile
361        50            55            60
364 Gly Ser Ala Leu Gln Phe Leu Ile Pro Arg Leu Pro Ser Phe Pro Thr
365 65            70            75            80
368 Gln Arg Thr Ser Lys Thr Leu Lys Val Leu Thr Pro Pro Ile Thr His
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 04/05/2007
PATENT APPLICATION: **US/10/763,976B**   TIME: 10:25:19

Input Set : **A:\960296.00463.txt**
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<u>Invalid <213> Response:</u>
**Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.**

Seq#:1,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29

VERIFICATION SUMMARY   DATE: 04/05/2007
PATENT APPLICATION: **US/10/763,976B**   TIME: 10:25:19

Input Set : **A:\960296.00463.txt**
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